SEQUENCE LISTING

- <110> Peltz, Stuart Czaplinski, Kevin Dinman, Jonathan D.
- <120> A SUBFAMILY OF RNA HELICASES WHICH ARE MODULATORS OF THE FIDELITY OF TRANSLATION TERMINATION AND USES THEREOF
- <130> 601-1-85N
- <140> 09/359,268
- <141> 1999-07-22
- <150> 60/093,685
- <151> 1998-07-22
- <160> 32

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- <170> PatentIn Ver. 2.0
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Ala	Ser	Thr	Leu	Val 165	Pro	Leu	Ser	Leu	Pro 170	Gly	Ile	Arg	Asn	Phe 175	Val
Phe	Val	Gly	Asp 180	Glu	Lys	Gln	Leu	Ser 185	Ser	Phe	Ser	Asn	Ile 190	Pro	Gln
Leu	Glu	Thr 195	Ser	Leu	Phe	Glu	Arg 200	Val	Leu	Ser	Asn	Gly 205	Thr	Tyr	Lys
Asn	Pro 210	Leu	Met	Leu	Asp	Thr 215	Gln	Tyr	Arg	Met	His 220	Pro	Lys	Ile	Ser
Glu 225	Phe	Pro	Ile	Lys	Lys 230	Ile	Tyr	Asn	Gly	Glu 235	Leu	Lys	Asp		Val 240
Thr	Asp	Glu	Gln	Lys 245	Ala	Trp	Pro	Gly	Val 250	Gln	His	Pro	Leu	Phe 255	Phe
Tyr	Gln	Cys	Asp 260	Leu	Gly	Pro	Glu	Ser 265	Arg	Val	Arg	Ser	Thr 270	Gln	Arg
Asp	Ile	Val 275	Gly	Phe	Thr	Tyr	Glu 280	Asn	Lys	His	Glu	Cys 285	Val	Glu	Ile
Val	Lys 290	Ile	Ile	Gln	Ile	Leu 295	Met	Leu	Asp	Lys	Lys 300	Val	Pro	Leu	Glu
Glu 305	Ile	Gly	Val	Ile	Thr 310	Pro	Tyr	Ser	Ala	Gln 315	Arg	Asp	Leu	Leu	Ser 320
Asp	Ile	Leu	Thr	Lys 325	Asn	Val	Val	Ile	Asn 330	Pro	Lys	Gln	Ile	Ser 335	Met
Gln	Gln	Glu	Tyr 340	Asp	Glu	Ile	Glu	Leu 345	Phe	Asn	Ala	Ala	Gly 350	Ser	Gln
Gly	Thr	Ala 355	Gly	Ser	Leu	Gln	Asn 360	Asn	Val	Ile	Asn	Ile 365	Ile	Asn	Gly
Leu	His 370	Val	Ala	Thr	Val	Asp 375	Ser	Phe	Gln	Gly	His 380	Glu	Lys	Ser	Phe

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Gln Leu Leu Lys Lys Gln Lys Ile Leu Ile Cys Ala Pro Ser Asn Ala 50 55 60

Ala Val Asp Glu Ile Cys Leu Arg Leu Lys Ser Gly Val Tyr Asp Lys
65 70 75 80

Gln Gly His Gln Phe Lys Pro Gln Leu Val Arg Val Gly Arg Ser Asp 85 90 95

Val Val Asn Val Ala Ile Lys Asp Leu Thr Leu Glu Glu Leu Val Asp
100 105 110

Lys Arg Ile Gly Glu Arg Asn Tyr Glu Ile Arg Thr Asp Pro Glu Leu 115 120 125

Glu Arg Lys Phe Asn Asn Ala Val Thr Lys Arg Arg Glu Leu Arg Gly
130 135 140

Lys Leu Asp Ser Glu Ser Gly Asn Pro Glu Ser Pro Met Ser Thr Glu 145 150 155 160

Asp Ile Ser Lys Leu Gln Leu Lys Ile Arg Glu Leu Ser Lys Ile Ile 165 170 175

Asn Glu Leu Gly Arg Asp Arg Asp Glu Met Arg Glu Lys Asn Ser Val

Asn Tyr Arg Asn Arg Asp Leu Asp Arg Arg Asn Ala Gln Ala His Ile Leu Ala Val Ser Asp Ile Ile Cys Ser Thr Leu Ser Gly Ser Ala His Asp Val Leu Ala Thr Met Gly Ile Lys Phe Asp Thr Val Ile Ile Asp Glu Ala Cys Gln Cys Thr Glu Leu Ser Ser Ile Ile Pro Leu Arg Tyr Gly Gly Lys Arg Cys Ile Met Val Gly Asp Pro Asn Gln Leu Pro Pro Thr Val Leu Ser Gly Ala Ala Ser Asn Phe Lys Tyr Asn Gln Ser Leu Phe Val Arg Met Glu Lys Asn Ser Ser Pro Tyr Leu Leu Asp Val Gln Tyr Arg Met His Pro Ser Ile Ser Lys Phe Pro Ser Ser Glu Phe Tyr Gln Gly Arg Leu Lys Asp Gly Pro Gly Met Asp Ile Leu Asn Lys Arg Pro Trp His Gln Leu Glu Pro Leu Ala Pro Tyr Lys Phe Phe Asp Ile Ile Ser Gly Arg Gln Glu Gln Asn Ala Lys Thr Met Ser Tyr Thr Asn Met Glu Glu Ile Arg Val Ala Ile Glu Leu Val Asp Tyr Leu Phe Arg Lys Phe Asp Asn Lys Ile Asp Phe Thr Gly Lys Ile Gly Ile Ile Ser Pro Tyr Arg Glu Gln Met Gln Lys Met Arg Lys Glu Phe Ala Arg Tyr Phe Gly Gly Met Ile Asn Lys Ser Ile Asp Phe Asn Thr Ile Asp Gly

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Asn Thr Asn Ile Ser Ile Met Arg Leu Gly Met Lys His Lys Val His 50 55 60

Pro Asp Thr Gln Lys Tyr Val Pro Asn Tyr Ala Ser Val Lys Ser Tyr 65 70 75 80

Asn Asp Tyr Leu Ser Lys Ile Asn Ser Thr Ser Val Val Ala Thr Thr 85 90 95

Cys Leu Gly Ile Asn Asp Ile Leu Phe Thr Leu Asn Glu Lys Asp Phe 100 105 110

Asp Tyr Val Ile Leu Asp Glu Ala Ser Gln Ile Ser Met Pro Val Ala 115 120 125

Leu Gly Pro Leu Arg Tyr Gly Asn Arg Phe Ile Met Val Gly Asp His 130 135 140

Tyr Gln Leu Pro Pro Leu Val Lys Asn Asp Ala Ala Arg Leu Gly Gly 145 150 155 160

Leu Glu Glu Ser Leu Phe Lys Thr Phe Cys Glu Lys His Pro Glu Ser 165 170 175

Val Ala Glu Leu Thr Leu Gln Tyr Arg Met Cys Gly Asp Ile Val Th	ır
Leu Ser Asn Phe Leu Ile Tyr Asp Asn Lys Leu Lys Cys Gly Asn As 195 200 205	in
Glu Val Phe Ala Gln Ser Leu Glu Leu Pro Met Pro Glu Ala Leu Se 210 215 220	r
Arg Tyr Arg Asn Glu Ser Ala Asn Ser Lys Gln Trp Leu Glu Asp II 225 230 235 24	
Leu Glu Pro Thr Arg Lys Val Val Phe Leu Asn Tyr Asp Asn Cys Pr 245 250 255	:0
Asp Ile Ile Glu Gln Ser Glu Lys Asp Asn Ile Thr Asn His Gly Gl 260 265 270	.u
Ala Glu Leu Thr Leu Gln Cys Val Glu Gly Met Leu Leu Ser Gly Va 275 280 285	,1
Pro Cys Glu Asp Ile Gly Val Met Thr Leu Tyr Arg Ala Gln Leu Ar 290 295 300	g
Leu Leu Lys Lys Ile Phe Asn Lys Asn Val Tyr Asp Gly Leu Glu Il 305 310 315 32	
Leu Thr Ala Asp Gln Phe Gln Gly Arg Asp Lys Lys Cys Ile Ile Il 325 330 335	.e
Ser Met Val Arg Arg Asn Ser Gln Leu Asn Gly Gly Ala Leu Leu Ly 340 345 350	s
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Thr	Lys 290	Ile	Pro	Leu	Ile	Trp 295	Tyr	Asp	Thr	Gln	Gly 300	Asp	Glu	Phe	Gln
Glu 305	Thr	Ala	Asp	Glu	Ala 310	Thr	Ile	Leu	Gly	Ser 315	Lys	Tyr	Asn	Glu	Gly 320
Glu	Ile	Ala	Ile	Val 325	Lys	Glu	His	Ile	Glu 330	Asn	Leu	Arg	Ser	Phe 335	Asn
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	370		Thr			375					380				
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- Thr Val Leu Ile Asp Glu Ser Thr Gln Ala Ser Glu Pro Glu Cys Leu 145 150 155 160
- Ile Pro Ile Val Lys Gly Ala Lys Gln Val Ile Leu Val Gly Asp His
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- Gln Gln Leu Gly Pro Val Ile Leu Glu Arg Lys Ala Ala Asp Ala Gly 180 185 190
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- Pro Ser Asn Met Phe Tyr Glu Gly Ser Leu Gln Asn Gly Val Thr Ile 225 230 235 240
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 325 330 335
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